FIG. 1

BLASTP - alignment of 359_protein (SEQ ID NO:2) against swiss|Q05017|PHLX_RABIT PHOSPHOLIPASE ADRAB-B PRECURSOR (EC 3.1.-.-).//:trembl|Z12841|OCPPHLIP_1

product: "Phospholipase"; O.cuniculus mRNA for phospholipase.

//:gp|Z12841|1690 product: "Phospholipase"; O.cuniculus mRNA for phospholipase.

This hit is scoring at : 0.0 (expectation value)
Alignment length (overlap) : 1217
Identities : 77 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb

```
Q:       1 EAWNSLLASSRYSEQESFTVVFQPFFYETTPSLHSEDPRLQDSTTLAWHLWNRMMEPAGE
             EAW:SLLASS:Y:.QESF.VVFQPFFYE:: S.   .:P LQD.TTLA .LWNRMMEP.G.
H:     259 EAWDSLLASSKYNTQESFAVVFQPFFYESSLSALLAEPPLQDPTTLALSLWNRMMEPIGR

           KDEPLSVKHGRPMKCPSQESPYLFSYRNSNYLTRLQKPQDKLGEKSIFLISLCVSFQVRE
           K:EP.S K. :P::CP:QESPYLF:YRNS..LTR:.:PQ.KL              :VRE
           KEEPFSEKERKPLRCPTQESPYLFTYRNSGQLTRVSQPQGKL--------------EVRE
```

prosite signature

```
           GAEIRCPDKDPSDTVPTSVHRLKPADINVIGALGDSLTAGNGAGSTPGNVLDVLTQYRGL
           G.EIRCPDKDPSD:VPTSVHRLKPADI.VIGA:GDSLTAGNGAGS.PGN:LDVLTQYRGL
           GTEIRCPDKDPSDSVPTSVHRLKPADIKVIGAMGDSLTAGNGAGSQPGNILDVLTQYRGL

           SWSVGGDENIGTVTTLANILREFNPSLKGFSVGTGKETSPNAFLNQAVAGGRAEDLPVQA
           SWSVGGD:NI.TVTTLANILREFNPSL:GFSVGTG:ET:..AF.NQAVAG.RA:.L  QA
           SWSVGGDQNISTVTTLANILREFNPSLQGFSVGTGRETTSQAFFNQAVAGARADGLIPQA

           RRLVDLMKNDTRIHFQEDWKIITLFIGGNDLCDFCNDLVHYSPQNFTDNIGKALDILHAE
           :RLV LMKNDTRI:FQEDWKIIT:FIGGNDLCDFCND V.YSPQNFTDNIG.ALDILHAE
           QRLVALMKNDTRINFQEDWKIITVFIGGNDLCDFCNDPVRYSPQNFTDNIGTALDILHAE

           VPRAFVNLVTVLEIVNLRELYQEKKVYCPRMILRSLCPCVLKFDDNSTELATLIEFNKKF
           :PRAFVNLV.VLEI .LRELYQE.KV CPRMILRSLCPCVLKFDDNSTE:A:LIE  K::
           IPRAFVNLVKVLEISKLRELYQETKVSCPRMILRSLCPCVLKFDDNSTEIASLIETIKEY

           QEKTHQLIESGRYDTREDFTVVVQPFFENVDMPKTSEGLPDNSFFAPDCFHFSSKSHSRA
           QE:T.QLI:SGRYDTR:DFTVV:QPFFE.V:MPKT.:GLPDNSFFAPDCFHFSSK:H:.A
           QERTQQLIDSGRYDTRDDFTVVLQPFFEKVNMPKTQDGLPDNSFFAPDCFHFSSKAHAHA

           ASALWNNMLEPVGQKTTRHKFENKINITCPNQFFWSLSTLRFWDLFYALRGHGTWLPCRD
           ASALWNNMLEPVGQKTT.:.FE..:NITCPNQ.:  LST.:      :::G.GTWLPCRD
           ASALWNNMLEPVGQKTTHNDFEGAVNITCPNQVWPFLSTYK-----NSVQGFGTWLPCRD
```

prosite signature

```
           RAPSALHPTSVHALRPADIQVVAALGDSLTAGNGIGSKPDDLPDVTTQYRGLSYSAGGDG
           R:PSA  PTSVHALRPADIQVVAALGDSLTAG GIGSKP:DL.D TTQYRGLSYS:GGDG
           RSPSASPPTSVHALRPADIQVVAALGDSLTAGIGIGSKPNDLSDGTTQYRGLSYSSGGDG

           SLENVTTLPNILREFNRNLTGYAVGTGDANDTNAFLNQAVPGAKAEDLMSQVQTLMQKMK
           SL:NVTTLPNILR:FN.NL.G:AVGTGDA:.TNAF.NQAVPGAKA.DLMSQVQTL:Q:MK
           SLDNVTTLPNILRQFNSNLMGFAVGTGDASGTNAFFNQAVPGAKARDLMSQVQTLVQRMK
```

DDHRVNFHEDWKVITVLIGGSDLCDYCTDSNLYSAANFVHHLRNALDVLHREVPRVLVNL
DDHRVNF.EDWKVITV IG.SDLCDYCTDSNLYSAANF..HLR:ALD.LHREVPR.LVNL
DDHRVNFQEDWKVITVQIGASDLCDYCTDSNLYSAANFYDHLRDALDALHREVPRALVNL

VDFLNPTIMRQVFLGNPDKCPVQQASVLCNCVLTLRENSQELARLEAFSRAYRSSMRELV
VDF:NP::.RQVFLGNPDKCPVQQAS.LCNCVL: RENS.ELARLEA.::AY:SS:RELV
VDFMNPSVTRQVFLGNPDKCPVQQASALCNCVLSPRENSYELARLEALAQAYQSSLRELV

GSGRYDTQEDFSVVLQPFFQNIQLPVLADGLPDTSFFAPDCIHPNQKFHSQLARALWTNM
SGRYDT:EDFSVVLQPFF.:IQLPVL.DG DTSFFAPDC:HPNQKFHSQL:RALW.NM
ESGRYDTREDFSVVLQPFFHSIQLPVLQDGRLDTSFFAPDCVHPNQKFHSQLSRALWRNM

LEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCTEWKAS
LEPLG.KT:.LDL.A.:.:TCPTQNEPFLRT RNS:YTYP :PA:ENWGSDFLCT.W.AS
LEPLGGKTDALDLTAAITLTCPTQNEPFLRTFRNSDYTYPSRPAVENWGSDFLCTAWNAS

NSVPTSVHQLRPADIKVVAALGDSLTVSMGARPNNSSDLPTSWRGLSWSIGGDGNLETHT
..VP.SVH:L:P.DIKVVAALGDSLT::MGARP:NSSD P. WRGLSWSIGGDG LETHT
RGVPNSVHELQPGDIKVVAALGDSLTLAMGARPSNSSDPPMFWRGLSWSIGGDGALETHT

TLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPDINLEK
TLPNILKKFNP :LGFST.T EGT.GLNVA.:GARA:DMPAQA DLVERM:NSP:I:LEK
TLPNILKKFNPSILGFSTGTLEGTMGLNVAVQGARAQDMPAQARDLVERMRNSPEIDLEK

DWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVMELASL
DWKLVTLF:G NDLCH:CENPE.. . EYVQHIQQALD:L EELPR.FVNVVEVMELA.L
DWKLVTLFVGGNDLCHFCENPEGSSEGEYVQHIQQALDVLYEELPRTFVNVVEVMELAGL

YQGQGGKCA-MLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQREDFA
:Q.QGG:CA :LAAQ::CTC.::SQSS:E.QELKKVNWNLQ.G:S..SY HQY.QREDFA
HQDQGGRCATLLAAQSHCTCFKYSQSSVEMQELKKVNWNLQSGLSRLSYSHQYVQREDFA

VVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRKTTSNN
VVVQPFFQNTL.PLN RGDTDLTFFS:DCFHFS:RGHAEMAIALWNNMLEPVG.KTTSNN
VVVQPFFQNTLVPLNGRGDTDLTFFSDDCFHFSERGHAEMAIALWNNMLEPVGHKTTSNN

FTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAP**EVLYWAVPVAAGVGLVVGIIGTVVV**W
FT:SR.KLKCPSP:SPYLYTLRNSRLLPDQAE. P.VLYWAVPVAAG.GL::GI:..V.
FTYSRTKLKCPSPDSPYLYTLRNSRLLPDQAEADPTVLYWAVPVAAGAGLLIGILAMVAG

RCRRGGRREDPPMSLRT 1216
R .R REDPP:SL.T
RGMRCRPREDPPLSLST 1456

Ser is the active site.

Transmembrane segment:

From 1176 to 1198: length= 23,

1176 VLYWAVPVAA GVGLVVGIIG TVV

FIG. 2.

Prosite search result

Access#	From->To	Name	Doc#
PS00016	1096->1099	RGD	PDOC00016
PS01098	150->161	LIPASE_GDSL_SER	PDOC00842
PS01098	502->513	LIPASE_GDSL_SER	PDOC00842

FIG. 3.

HMMPFAM - alignment of 359_protein (SEQ ID NO:3) against pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

```
This hit is scoring at : 168.6  Expect: 1e-46
Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Q:     149 VIGALGDSLTAGNGAGSTPGNVLDVLTQYRGLSWSVGGDENIGTVTTLANILREFNPSLK
             : ALGDSLT G.G GS.. .: D ..QYRGLS S  GD N... T.L.:IL.:
H:       1 kvvalGDSLtdgggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

           G---------FSVGTGKETSPNAFLNQAVAGGRAEDLPVQARRLVD--------LMKNDT
           G         F.VG. :E... . LN AV.G..AEDL  :. .L:D        M ..:
           gVgikeksilfrvgklqengsltglNfAvgGataedllkrlpnlldqvikksqykmygks

           RIHFQEDWKIITLFIGGNDLCDFCND      277
           R . Q:D .::T: :GGNDLCD: .D
           rkksqkdpdlvtielGgNDlcdyfrd      146
```

FIG. 4.

HMMPFAM - alignment of 359_protein (SEQ ID NO:2) against pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

This hit is scoring at : 172.2 Expect: 8.7e-48

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```
Q:    501 VVAALGDSLTAGNGIGSKPDDLPDVTTQYRGLSYSAGGDGSLENVTTLPNILREFNRNLT
           V.ALGDSLT G.G GS:...L.D  .QYRGLS S: GDG:..N T.LP:IL.:      .
H:      1 kvvalGDSLtdgggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

          G---------YAVGTGDANDTNAFLNQAVPGAKAEDLMSQVQTLMQ--------KMKDDH
          G         :.VG. ..N.: . LN AV GA.AEDL:.::..L:.        KM ...
          gVgikeksilfrvgklqengsltglNfAvgGataedllkrlpnlldqvikksqykmygks

          RVNFHEDWKVITVLIGGSDLCDYCTD     629
          R . .:D .::T: :GG:DLCDY .D
          rkksqkdpdlvtielGgNDlcdyfrd     146
```

FIG. 5

HMMPFAM - alignment of 359_protein (SEQ ID NO:2) against pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

```
This hit is scoring at : 155.2 Expect: 1.1e-42
Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Q:     857 VVAALGDSLTVSMGARPNN--SSDLPTSWRGLSWSIGGDGNLETHTTLPNILKKFNPYLL
            V.ALGDSLT . G  ..:   .D  ..:RGLS S  GDGN... T.LP:IL.K   . L
H:       1 kvvalGDSLtdgggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

           G------------FSTSTWEGTAGLNVAAEGARARDMPAQAWDLVE--------RMKNSP
           G             ....  ...GLN.A. GA.A.D: .:. :L::        :M ...
           gVgikeksilfrvgklqengsltglNfAvgGataedllkrlpnlldqvikksqykmygks

           DINLEKDWKLVTLFIGVNDLCHYCEN    980
             . :KD .LVT: :G NDLC.Y .:
           rkksqkdpdlvtielGgNDlcdyfrd    146
```

SEQUENCE LISTING

SEQ ID NO:1

gaagcctgga acagcctcct ggcctccagc aggtacagtg agcaggagtc cttcaccgtg

gttttccagc ctttcttcta tgagaccacc ccatctctac actcggagga cccccgactc

caggattcta ccacgctggc ctggcatctc tggaatagga tgatggagcc agcaggagag

aaagatgagc cattgagtgt aaaacacggg aggccaatga agtgtccctc tcaggagagc

ccctatctgt tcagctacag aaacagcaac tacctgacca gactgcagaa accccaagac

aagcttggag aaaaatccat tttccttatt tccctgtgtg tctcatttca ggtaagagaa

ggagcggaaa tcagatgtcc tgacaaagac ccctccgata cggttcccac ctcagttcat

aggctgaagc cggctgacat caacgtaatt ggagccctgg gtgactctct cacggcaggc

aatggggccg ggtccacacc tgggaacgtc ttggacgtct tgactcagta ccgaggcctg

tcctggagcg tcggcggaga tgagaacatc ggcaccgtta ccaccctggc gaacatcctc

cgggaattca acccttccct gaagggcttc tctgttggca ctgggaaaga aaccagtcct

aatgccttct taaaccaggc tgtggcagga ggccgagctg aggatctacc tgtccaggcc

aggaggctgg tggacctgat gaagaatgac acgaggatac actttcagga agactggaag

ataataaccc tgtttatagg cggcaatgac ctctgtgatt tctgcaatga tctggtccac

tattctcccc agaacttcac agacaacatt ggaaaggccc tggacatcct ccatgctgag

gttcctcggg catttgtgaa cctggtgacg gtgcttgaga tcgtcaacct gagggagctg

taccaggaga aaaaagtcta ctgcccaagg atgatcctca ggtctctgtg tccctgtgtc

ctgaagtttg atgataactc aacagaactt gctaccctca tcgaattcaa caagaagttt

caggagaaga cccaccaact gattgagagt gggcgatatg acacaaggga agattttact

gtggttgtgc agccgttctt tgaaaacgtg gacatgccaa agacctcgga aggattgcct

gacaactctt tcttcgctcc tgactgtttc cacttcagca gcaagtctca ctcccgagca

gccagtgctc tctggaacaa tatgctggag cctgttggcc agaagacgac tcgtcataag

tttgaaaaca agatcaatat cacatgtccg aaccagtttt tctggtccct ttcaaccctg

agattctggg atttgttcta tgcccttagg ggtcatggga cctggctgcc atgcagggac

agagcccctt ctgccttgca ccctacctca gtgcatgccc tgagacctgc agacatccaa

gttgtggctg ctctgggggа ttctctgacc gctggcaatg gaattggctc caaaccagac

gacctccccg atgtcaccac acagtatcgg ggactgtcat acagtgcagg aggggacggc

tccctggaga atgtgaccac cttacctaat atccttcggg agtttaacag aaacctcaca
ggctacgccg tgggcacggg tgatgccaat gacacgaatg cattcctcaa tcaagctgtt
cccggagcaa aggctgagga tcttatgagc caagtccaaa ctctgatgca gaagatgaaa
gatgatcata gagtaaattt ccatgaagac tggaaggtca tcacagtgct gatcggaggc
agcgatttat gtgactactg cacagattcg aatctgtatt ctgcagccaa ctttgttcac
catctccgca atgccttgga cgtcctgcat agagaggtgc ccagagtcct ggtcaacctc
gtggacttcc tgaaccccac tatcatgcgg caggtgttcc tgggaaaccc agacaagtgc
ccagtgcagc aggccagcgt tttgtgtaac tgcgttctga ccctgcggga gaactcccaa
gagctagcca ggctggaggc cttcagccga gcctaccgga gcagcatgcg cgagctggtg
gggtcaggcc gctatgacac gcaggaggac ttctctgtgg tgctgcagcc cttcttccag
aacatccagc tccctgtcct ggcggatggg ctcccagata cgtccttctt tgccccagac
tgcatccacc caaatcagaa attccactcc cagctggcca gagccctttg gaccaatatg
cttgaaccac ttggaagcaa aacagagacc ctggacctga gagcagagat gcccatcacc
tgtcccactc agaatgagcc cttcctgaga acccctcgga atagtaacta cacgtacccc
atcaagccag ccattgagaa ctggggcagt gacttcctgt gtacagagtg gaaggcttcc
aatagtgttc caacctctgt ccaccagctc cgaccagcag acatcaaagt ggtggccgcc
ctgggtgact ctctgactgt gagtatggga gctcgaccaa acaactccag tgacctaccc
acatcttgga ggggactctc ttggagcatt ggaggggatg ggaacttgga gactcacacc
acactgccca acattctgaa gaagttcaac ccttacctcc ttggcttctc taccagcacc
tgggaggggа cagcaggact aaatgtggca gcggaagggg ccagagctag ggacatgcca
gcccaggcct gggacctggt agagcgaatg aaaaacagcc ccgacatcaa cctggagaaa
gactggaagc tggtcacact cttcattggg gtcaacgact tgtgtcatta ctgtgagaat
ccggaggccc acttggccac ggaatatgtt cagcacatcc aacaggccct ggacatcctc
tctgaggagc tcccaagggc tttcgtcaac gtggtggagg tcatggagct ggctagcctg
taccagggcc aaggcgggaa atgtgccatg ctggcagctc agaacaactg cacttgcctc

SEQ ID NO:2

EAWNSLLASS RYSEQESFTV VFQPFFYETT PSLHSEDPRL QDSTTLAWHL WNRMMEPAGE
KDEPLSVKHG RPMKCPSQES PYLFSYRNSN YLTRLQKPQD KLGEKSIFLI SLCVSFQVRE
GAEIRCPDKD PSDTVPTSVH RLKPADINVI GALGDSLTAG NGAGSTPGNV LDVLTQYRGL
SWSVGGDENI GTVTTLANIL REFNPSLKGF SVGTGKETSP NAFLNQAVAG GRAEDLPVQA

RRLVDLMKND TRIHFQEDWK IITLFIGGND LCDFCNDLVH YSPQNFTDNI GKALDILHAE

VPRAFVNLVT VLEIVNLREL YQEKKVYCPR MILRSLCPCV LKFDDNSTEL ATLIEFNKKF

QEKTHQLIES GRYDTREDFT VVVQPFFENV DMPKTSEGLP DNSFFAPDCF HFSSKSHSRA

ASALWNNMLE PVGQKTTRHK FENKINITCP NQFFWSLSTL RFWDLFYALR GHGTWLPCRD

RAPSALHPTS VHALRPADIQ VVAALGDSLT AGNGIGSKPD DLPDVTTQYR GLSYSAGGDG

SLENVTTLPN ILREFNRNLT GYAVGTGDAN DTNAFLNQAV PGAKAEDLMS QVQTLMQKMK

DDHRVNFHED WKVITVLIGG SDLCDYCTDS NLYSAANFVH HLRNALDVLH REVPRVLVNL

VDFLNPTIMR QVFLGNPDKC PVQQASVLCN CVLTLRENSQ ELARLEAFSR AYRSSMRELV

GSGRYDTQED FSVVLQPFFQ NIQLPVLADG LPDTSFFAPD CIHPNQKFHS QLARALWTNM

LEPLGSKTET LDLRAEMPIT CPTQNEPFLR TPRNSNYTYP IKPAIENWGS DFLCTEWKAS

NSVPTSVHQL RPADIKVVAA LGDSLTVSMG ARPNNSSDLP TSWRGLSWSI GGDGNLETHT

TLPNILKKFN PYLLGFSTST WEGTAGLNVA AEGARARDMP AQAWDLVERM KNSPDINLEK

DWKLVTLFIG VNDLCHYCEN PEAHLATEYV QHIQQALDIL SEELPRAFVN VVEVMELASL

YQGQGGKCAM LAAQNNCTCL RHSQSSLEKQ ELKKVNWNLQ HGISSFSYWH QYTQREDFAV

VVQPFFQNTL TPLNERGDTD LTFFSEDCFH FSDRGHAEMA IALWNNMLEP VGRKTTSNNF

THSRAKLKCP SPESPYLYTL RNSRLLPDQA EEAPEVLYWA VPVAAGVGLV VGIIGTVVWR

CRRGGRREDP PMSLRT

SEQ ID NO:3
Q05017

MALWPSVFLL GLLPLLGRGA DQIQTSSGKN TLEGQLWPES LKTFPFPCDP KTLAESVPSE

SVHSLRPSDI KFVAAIGNVE TAPDSGADDL EEQDGTEKRP EQACMGVVTV LSDIIGRFSP

SALMPLCPET RLVPRGGAED LWMQATELVR SMRENPQLDF EHDWKLINVF FSNTSQCFPC

PSAQQKGLVL GGMDKLTRTL DYLQQEVPKA FVNLVDLSEL AAFSRWRQGA QLSPAAEPCR

CLRETSQLTK VLTQWSYLEA WDSLLASSKY NTQESFAVVF QPFFYESSLS ALLAEPPLQD

PTTLALSLWN RMMEPIGRKE EPFSEKERKP LRCPTQESPY LFTYRNSGQL TRVSQPQGKL

EVREGTEIRC PDKDPSDSVP TSVHRLKPAD IKVIGAMGDS LTAGNGAGSQ PGNILDVLTQ

YRGLSWSVGG DQNISTVTTL ANILREFNPS LQGFSVGTGR ETTSQAFFNQ AVAGARADGL

IPQAQRLVAL MKNDTRINFQ EDWKIITVFI GGNDLCDFCN DPVRYSPQNF TDNIGTALDI

LHAEIPRAFV NLVKVLEISK LRELYQETKV SCPRMILRSL CPCVLKFDDN STEIASLIET

IKEYQERTQQ LIDSGRYDTR DDFTVVLQPF FEKVNMPKTQ DGLPDNSFFA PDCFHFSSKA

HAHAASALWN NMLEPVGQKT THNDFEGAVN ITCPNQVWPF LSTYKNSVQG FGTWLPCRDR

SPSASPPTSV HALRPADIQV VAALGDSLTA GIGIGSKPND LSDGTTQYRG LSYSSGGDGS

LDNVTTLPNI LRQFNSNLMG FAVGTGDASG TNAFFNQAVP GAKARDLMSQ VQTLVQRMKD

DHRVNFQEDW KVITVQIGAS DLCDYCTDSN LYSAANFYDH LRDALDALHR EVPRALVNLV

DFMNPSVTRQ VFLGNPDKCP VQQASALCNC VLSPRENSYE LARLEALAQA YQSSLRELVE

SGRYDTREDF SVVLQPFFHS IQLPVLQDGR LDTSFFAPDC VHPNQKFHSQ LSRALWRNML

EPLGGKTDAL DLTAAITLTC PTQNEPFLRT FRNSDYTYPS RPAVENWGSD FLCTAWNASR

GVPNSVHELQ PGDIKVVAAL GDSLTLAMGA RPSNSSDPPM FWRGLSWSIG GDGALETHTT

LPNILKKFNP SILGFSTGTL EGTMGLNVAV QGARAQDMPA QARDLVERMR NSPEIDLEKD

WKLVTLFVGG NDLCHFCENP EGSSEGEYVQ HIQQALDVLY EELPRTFVNV VEVMELAGLH

QDQGGRCATL LAAQSHCTCF KYSQSSVEMQ ELKKVNWNLQ SGLSRLSYSH QYVQREDFAV

VVQPFFQNTL VPLNGRGDTD LTFFSDDCFH FSERGHAEMA IALWNNMLEP VGHKTTSNNF

TYSRTKLKCP SPDSPYLYTL RNSRLLPDQA EADPTVLYWA VPVAAGAGLL IGILAMVAGR

GMRCRPREDP PLSLSTGL

SEQ ID NO:4
embl|AA418082|HS1213495 . (EST)
TAAAATAGCTTTGGACTTTATTTAAATGTATCCATTCCAGGAGCATAGGCCTGGAAGAAG

CCCAGGCCCCAAGAAGTTGTGACTGTCCCCTGGGCTTCCTATGGCACCAGGCATTGAAGC

ATGTCCTGGTGGCCGGGAGTGGCTGGGGCAGAGGGCAGTGAAGAGGGTGGCTATAGGGAG

TTTAGGGTGAGGACCCACCCCCGGGCCTAGAGGGCACCAGTGCGCAGGCTCATTGGAGGA

TCTTCCCTCCGGCCACCTCTCCTGCACCTCCAGACCACTGTCCCGATGATGCCCACCACA

AGGCCGACTCCCGCTGCCACTGGGACAGCCCAGTAGAGCACCTCGGGGGCTTCTTCAGCC

TGGTCTGGGAGCAGTCGGCTGTTCCGCAGGGTGTAGAGGTAAGGGCTCTCAGGAGAGGGG

CACTTGAGTTTGGCTCGGCTGTGGGTGAAGTTGTTGGAGGTAGTCTTGCGGCCCACTGGT

TCCAGCATGTTGTTCCAGAGTGCGATGGCCATCTCGGCATGCCCGCGGTCTGAGAAGTGA
AAACAGTCCTCGGAGAAGAAGGTGAGGTCAGTGTCCCCTCTCT

SEQ ID NO:5
genbank|AW851123|AW851123 . (EST)
GTCCCCTGTCTTGATGGGCTGCATAGAGAGGTGCCCAGAGTCCTGGTCAACCTCGTGGAC

TTCCTGAACCCCACTATCATGCGGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTG

CAGCAGGCCAGCGTTTTGTGTAACTGCGTTCTGACCCTGCGGGAGAACTCCCAAGAGCTA

GCCAGGCTGGAGGCCTTCAGCCGAGCCTACCGGAGCAGCATGCGCGAGCTGGTGGGGTCA

GGCCGCTATGACACGCAGGAGGACTTCTCTGTGGTGCTGCAGCCCTTCTTCCAGAACATC

CAGCTCCCTGTCCTGGCGGATGGGCTCCCAGATACGTCCTTCTTTGCCCCAGACTGCATC

CACCCAAATCAGAAATTCCACTCCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAA

CCACTTGGAAGCAAAACAGAGACCCTGGACCTGAGAGCAGAGATGCCCATCACCTGTCCC

ACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAAGAACTACACGTACCCCATCAAG

CCAGCCATTGAGAACTGGGGCAGTGACTTTCTGTGTACAGAAGTGGAAGCTTCCAATAGT
GGTCCAAT

SEQ ID NO:6
embl|AA418228|HS1213659 . (EST)
CCCAGCTGGCAGAGCCTTTGGACCAATATGCTTGAACCACTTGGAAGCAAAACAGAGACC

CTGGACCTGAGAGCAGAGATGCCCATCACCTGTCCCACTCAGAATGAGCCCTTCCTGAGA

ACCCCTCGGAATAGTAACTACACGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCAGT

GACTTCCTGTGTACAGAGTGGAAGGCTTCCAATAGTGTTCCAACCTCTGTCCACCAGCTC
CGACCAGCAGACATCAAAGTGGTGG

SEQ ID NO:7
embl|AI952246|AI952246 . (EST)
TAAAATAGCTTTGGACTTTATTTAAATGTATCCATTCCAGGAGCATAGGCCTGGAAGAAG

CCCAGGCCCCAAGAAGTTGTGACTGTCCCCTGGGCTTCCTAGGGCACCAGGCATTGAAGC

ATGTCCTGGTGGCCGGGAGTGGCTGGGGCAGAGGGCGGTGAAGAGGGTGGCTATAGGGAG

TTTAGGGTGAGGACCCACCCCCGGGCCTAGAGGGCCACAGTGCGCAGGCTCATTGGAGGA

TCTTCCCTCCGGCCACCTCTCCTGCACCTCCAGACCACTGTCCCGATGATGCCCACCACA

AGGCCGACTCCCGCTGCCACTGGGACAGCCCAGTAGAGCACCTCGGGGGCTTCTTCAGCC

TGGTCTGGGAGCAGTCGGCTGTTCCGCAGGGTGTAGAGGTAAGGGCTCTCAGGAGAGGNG
CACTTGAGTTTGGCTCGGCTGTGGGT